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Reviewer Comments:
<210> 2
<211> 1588
<212> DNA
<213> Human

<220>
<221> CDS
<222> (1)...(1059)

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tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc 180
ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc 360
tac agc agt gtc ctc atc ctg gcc ttc atc agt ctg gac cgc tac 405
ctg gcc atc gtc cac gcc acc aac agt cag agg cca agg aag ctg 450
ttg gct gaa aag gtg gtc tat gtt ggc gtc tgg atc cct gcc ctc 495
ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc aag 675
ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
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tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810
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gca ctc acc tct gtg agc aga ggg tcc agc ctc aag atc ctc tcc 990
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ggagtgggtt gatttcagca cctacagtgt acagtcttgt attaagttgt taataaaagt 1565
acatgttaaa cttaaaaaaa aaa 1588

In a coding sequence, Per above attach please insert (3) letter codings for amino acids below the corresponding nucleotide triplets.

Numeric identifier <213> can only be one of three choices, “Scientific name, i.e. Genus/species, Unknown or Artificial Sequence.” For all sequences using “Unknown or Artificial sequence”, for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. To explain the source, if the sequence is put together from several organisms, please list those organisms. If the sequence is made in the laboratory, please indicate that the sequence is synthesized. Please check for similar errors in subsequent sequences and make necessary changes.

<210>10
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> added peptide

<400> 10
Arg Leu Lys Met

Per above is an insufficient response for numeric identifier <223>. Please explain the source of the genetic material. When using “Unknown”

for numeric identifier <213>, please provide as much taxonomic information, as possible, about the organism from which the genetic material was extracted. If the genetic material was extracted from a sample in which there was an unknown variety of organisms, please explain where the sample was taken, for example a soil sample. These errors appear in other sequences in the sequence listing. Please make all necessary changes.

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Validated By CRFValidator v 1.0.3

Application No: 10785230 Version No: 3.0

Input Set:

Output Set:

Started: 2008-10-22 15:28:17.780
Finished: 2008-10-22 15:28:18.718
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 938 ms
Total Warnings: 12
Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code		Error Description
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W	402	Undefined organism found in <213> in SEQ ID (2)
W	402	Undefined organism found in <213> in SEQ ID (3)
W	402	Undefined organism found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
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W	213	Artificial or Unknown found in <213> in SEQ ID (7)
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W	213	Artificial or Unknown found in <213> in SEQ ID (9)
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W	213	Artificial or Unknown found in <213> in SEQ ID (11)
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SEQUENCE LISTING

<110> KISHIMOTO, Tadamitsu
NAGASAWA, Takashi
TACHIBANA, Kazunobu

<120> Inhibiting vascularization using antibodies to CXCR4 and SDF-1

<130> 46124-5042-US01

<140> 10785230
<141> 2004-02-25

<150> US 09/646,785
<151> 2001-02-16

<150> PCT/JP99/01448
<151> 1999-03-23

<150> JP10/95448
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Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
 50                  55                  60
Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys
 65                  70                  75
Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr
 80                  85                  90
Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly
 95                 100                 105
Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
110                 115                 120
Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr
125                 130                 135
Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
140                 145                 150
Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu
155                 160                 165
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Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp
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                230                 235                 240
Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
                245                 250                 255
Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile
                260                 265                 270
Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser
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Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
                290                 295                 300
Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His
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Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser
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<222> (1)...(1059)

<400> 2

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tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc 180
ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc 360
tac agc agt gtc ctc atc ctg gcc ttc atc agt ctg gac cgc tac 405
ctg gcc atc gtc cac gcc acc aac agt cag agg cca agg aag ctg 450
ttg gct gaa aag gtg gtc tat gtt ggc gtc tgg atc cct gcc ctc 495
ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc aag 675
ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac 765
tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810
aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
atc acc gag gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc 900
ctc tat gct ttc ctt gga gcc aaa ttt aaa acc tct gcc cag cac 945
gca ctc acc tct gtg agc aga ggg tcc agc ctc aag atc ctc tcc 990
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gtggccaagt tcttagttgc tgtatgtctc gtggtaggac tgtagaaaag ggaactgaac 1325
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Phe Arg Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr
35 40 45
Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu
50 55 60
Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr
65 70 75
Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
80 85 90
Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp Trp Tyr
95 100 105
Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
110 115 120
Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
125 130 135
Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg
140 145 150
Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro
155 160 165
Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser
170 175 180
Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg
185 190 195
Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His
200 205 210
Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys
215 220 225
Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
230 235 240
Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
245 250 255
Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser
260 265 270
Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser
275 280 285

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Ile Val His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe
                290                 295                 300
His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys
                305                 310                 315
Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met Ser Arg Gly
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Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser
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<210> 4
<211> 1758
<212> DNA
<213> Mus

<220>
<221> CDS
<222> (1)...(1080)

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gtg atc ctg gtc atg ggt tac cag aag aag cta agg agc atg acg 225
gac aag tac cgg ctg cac ctg tca gtg gct gac ctc ctc ttt gtc 270
atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac tgg tac 315
ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act gtc 360
aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac 405
cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg 450
aaa ctg ctg gct gaa aag gca gtc tat gtg ggc gtc tgg atc cca 495
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ttc atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc 855
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cac tgt tgc ctg aac ccc atc ctc tat gcc ttc ctc ggg gcc aag 945
ttc aaa agc tct gcc cag cat gca ctc aac tcc atg agc aga ggc 990
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<212> PRT
<213> Artificial Sequence

<220>
<223> Ligand peptide

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35 40 45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
50 55 60
Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
65 70 75
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys
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<212> DNA
<213> Mus

<220>
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<222> (471)...(743)

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<220>
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35 40 45
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
50 55 60
Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
65 70 75
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<210> 8
<211> 1781
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<220>
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<222> (82)...(351)

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ctc tgc atc agt gac ggt aaa cca gtc agc ctg agc tac cga tgc 171
ccc tgc cgg ttc ttc gag agc cac atc gcc aga gcc aac gtc aag 216
cat ctg aaa atc ctc aac act cca aac tgt gcc ctt cag att gtt 261
gca cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aaa 306
tta aag tgg atc caa gag tac ctg gag aaa gct tta aac aag taa 351
gcacaacagc ccaaaggact ttccagtaga cccccgagga aggctgacat ccgtgggaga 411
tgcaagggca gtggtgggga ggagggcctg aaccctggcc aggatggccg gcgggacagc 471
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